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Search Results -

Term	Documents
435/6[USPT]	9615
435/6S	0
702/19[USPT]	267
702/19S	0
702/20[USPT]	98
702/20S	0
((((702/20[CCLS]) OR (702/19[CCLS])) OR (435/6[CCLS])) AND 9).USPT.	0
(L9 AND (435/6[CCLS] OR 702/19[CCLS] OR 702/20[CCLS])).USPT.	0

Database: US Patents Full-Text Database
US Pre-Grant Publication Full-Text Database
JPO Abstracts Database
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09/758872

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB,JPAB,EPAB,DWPI,TDBD; PLUR=YES; OP=OR			
L1	computer$ and (dna$ near5 chip$)	801	L1
L2	computer$ and (dna$ near probe)	5132	L2
L3	(probe near chip$) and dna$ and computer$	126	L3
L4	(probe near5 chip$) and dna$ and computer$	451	L4
L5	l1 or l4	1012	L5
L6	hybridi$	59539	L6
L7	l5 and hybridi$	918	L7
DB=USPT; PLUR=YES; OP=OR			
L8	L7	441	L8
DB=PGPB; PLUR=YES; OP=OR			
L9	L7	470	L9
DB=JPAB; PLUR=YES; OP=OR			
L10	l7	0	L10
DB=EPAB; PLUR=YES; OP=OR			
L11	l7	0	L11
DB=DWPI; PLUR=YES; OP=OR			
L12	l7	7	L12
DB=TDBD; PLUR=YES; OP=OR			
L13	l7	0	L13
DB=USPT; PLUR=YES; OP=OR			
L14	l8 and (435/6[ccls] or 702/19[ccls] or 702/20[ccls])	291	L14
L15	L14 and (correlat$)	170	L15
L16	l9 and (435/6[ccls] or 702/19[ccls] or 702/20[ccls])	0	L16

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END OF SEARCH HISTORY

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FILE 'HOME' ENTERED AT 12:48:10 ON 25 SEP 2002

=> le caplus
LE IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter "HELP COMMANDS" at an arrow prompt (=>).

=> file caplus
COST IN U.S. DOLLARS SINCE FILE TOTAL ENTRY SESSION
FULL ESTIMATED COST 0.21 0.21

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FILE COVERS 1907 - 25 Sep 2002 VOL 137 ISS 13
FILE LAST UPDATED: 24 Sep 2002 (20020924/ED)
This file contains CAS Registry Numbers for easy and accurate substance identification.

CAS roles have been modified effective December 16, 2001. Please
check your SDI profiles to see if they need to be revised. For information on CAS roles, enter HELP ROLES at an arrow prompt or use
the CAS Roles thesaurus (/RL field) in this file.

=> s (computer? and (dna# 5w chip?))/bi,ab 240057
COMPUTER?/BI 175608 COMPUTER?/AB 578785 DNA#/BI 1152 5W/BI 60237 CHIP?/BI 0 DNA# 5W CHIP?/BI
((DNA#(W)5W(W)CHIP?)/BI) 474939 DNA#/AB 1108 5W/AB 53751 CHIP?/AB 0 DNA# 5W CHIP?/AB
((DNA#(W)5W(W)CHIP?)/AB)
L1 0 (COMPUTER? AND (DNA# 5W CHIP?))/BI,AB

=> s (computer? and (dna# 5a chip?))/bi,ab 240057
COMPUTER?/BI 175608 COMPUTER?/AB 578785 DNA#/BI 11697 5A/BI 60237 CHIP?/BI 0 DNA# 5A CHIP?/BI
((DNA#(W)5A(W)CHIP?)/BI) 474939 DNA#/AB 8435 5A/AB 53751 CHIP?/AB 0 DNA# 5A CHIP?/AB
((DNA#(W)5A(W)CHIP?)/AB)
L2 0 (COMPUTER? AND (DNA# 5A CHIP?))/BI,AB

=> s (computer? and (dna(5a)chip?))/bi,ab 240057
COMPUTER?/BI 175608 COMPUTER?/AB 574766 DNA/BI 469207 DNA/AB 60237 CHIP?/BI 53751 CHIP?/AB 1141 DNA(5A)CHIP?
L3 62 (COMPUTER? AND (DNA(5A)CHIP?))/BI,AB

=> s ((computer? and (probe(5a)chip?) and dna#)/bi,ab
UNMATCHED LEFT PARENTHESIS '((COMPUTER?'
The number of right parentheses in a query must be equal to the number of left parentheses.

=> ((computer? and (probe(5a)chip?) and dna#))/bi,ab
((COMPUTER? IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter "HELP COMMANDS" at an arrow prompt (=>).

=> s ((computer? and (probe(5a)chip?) and dna#))/bi,ab
240057 COMPUTER?/BI 175608 COMPUTER?/AB 172249 PROBE/BI 148725 PROBE/AB 60237 CHIP?/BI 53751 CHIP?/AB 157 PROBE(5A)CHIP? 578785 DNA#/BI 474939 DNA#/AB
L4 6 ((COMPUTER? AND (PROBE(5A)CHIP?) AND DNA#))/BI,AB

=> d his
(FILE 'HOME' ENTERED AT 12:48:10 ON 25 SEP 2002)
FILE 'CAPLUS' ENTERED AT 12:48:22 ON 25 SEP 2002
L1 0 S (COMPUTER? AND (DNA# 5W CHIP?))/BI,AB
L2 0 S (COMPUTER? AND (DNA# 5A CHIP?))/BI,AB
L3 62 S (COMPUTER? AND (DNA(5A)CHIP?))/BI,AB
L4 6 S ((COMPUTER? AND (PROBE(5A)CHIP?) AND DNA#))/BI,AB

=> s l3 or l4
L5 64 L3 OR L4

=> s l5 not 2002/py 703789 2002/PY
L6 44 L5 NOT 2002/PY

=> s l6 not 2001/py 1041898 2001/PY

L7 29 L6 NOT 2001/PY

=> d l7 1-29 bib ab

L7 ANSWER 1 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 2001:341205 CAPLUS
DN 135:76452
TI Data submission system for cyanobacterial ***DNA*** ***chip*** consortium
AU Uchiyama, Ikuo; Miwa, Tomoki; Nishide, Hiroyo; Suzuki, Iwane; Omata, Tatsuo; Ikeuchi, Masahiko; Murata, Norio; Kanehisa, Minoru
CS National Institute for Basic Biology, Research Center for Computational Science, Okazaki National Research Institutes, Okazaki, 444-8585, Japan
SO Genome Informatics Series (2000), 11(Genome Informatics 2000), 235-236 CODEN: GINSE9; ISSN: 0919-9454
PB Universal Academy Press
DT Journal
LA English
AB A DNA microarray is an extremely useful tool for functional genomics by surveying genome-wide gene expression changes in cells under different conditions. A cyanobacterial ***DNA*** ***chip*** consortium established under the Genome Frontier Project, consists of Japanese cyanobacterial researchers with a wide range of interests. In each member's lab., expts. are underway using the same chip on which segments of almost all ORFs identified in Synechocystis sp. PCC6803 genome are spotted, but using various materials subjected to changes in different environmental conditions such as temp., light intensity or CO2 concn. The data submission system for this consortium is hereby presented. The system accepts and manages data about exptl. conditions and relates them to the submitted expression data file produced from the image anal. software.
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 2 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 2001:341182 CAPLUS
DN 136:96791
TI Intelligent ***DNA*** ***chips*** : logical operation of gene expression profiles on DNA ***computers***
AU Sakakibara, Yasubumi; Suyama, Akira
CS Department of Information Sciences, Tokyo Denki University, Saitama, 350-0394, Japan
SO Genome Informatics Series (2000), 11(Genome Informatics 2000), 33-42 CODEN: GINSE9; ISSN: 0919-9454
PB Universal Academy Press
DT Journal
LA English
AB The authors propose a new type of ***DNA*** ***chips*** with logical operations executable. In DNA computing researches, some methods have been developed to represent and evaluate Boolean functions on DNA strands. By employing the evaluation methods, the authors are able to deal with logical operations such as logical-"and" and logical-"or" for gene expressions. By combining with the DNA Coded No. method, the authors implement universal ***DNA*** ***chips*** which not only detect gene expressions but also find logical formulas of gene expressions. An important advantage of the intelligent ***DNA*** ***chip*** is that the intensity of the fluorescence at each element is not only proportional to the expression level of the genes in the sample but also proportional to the satisfiability level of the Boolean formula at the element with the gene expression pattern. These features of the intelligent ***DNA*** ***chip*** and the DCN method allow the authors more quant. analyses of gene expression profiles and the logical operations.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 3 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 2001:213808 CAPLUS
DN 136:1135
TI Design and on-chip synthesis technology of oligonucleotide microarray
AU Lu, Zuhong; Zhao, Yujie; He, Nongyao; Sun, Xiao
CS National Laboratory for Molecular and Biomolecular Electronics, Southeast University, Nanjing, 210096, Peop. Rep. China
SO Proceedings of SPIE-The International Society for Optical Engineering (2000), 4224(Biomedical Photonics and Optoelectronic Imaging), 118-121 CODEN: PSISDG; ISSN: 0277-786X
PB SPIE-The International Society for Optical Engineering
DT Journal; General Review
LA English
AB A review, with refs., discussing genechip engineering including a set of techniques, such as chip fabrication, target gene prepn. and hybridization, pattern detection and processing, bioinformatics related to the probe design and data anal. Some results in on-chip synthesizing the oligonucleotides microarray with mol. stamping or microfluidic molds, and developing software for probe designs are presented.
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 4 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 2001:41344 CAPLUS
DN 135:237145
TI Genomics and proteomics tools for the clinic
AU Rudert, Fritz
CS Xerion Pharmaceuticals GmbH, Munich, D-82152, Germany
SO Current Opinion in Molecular Therapeutics (2000), 2(6), 633-642 CODEN: CUOTFO; ISSN: 1464-8431
PB PharmaPress Ltd.
DT Journal; General Review
LA English
AB A review with 59 refs. The sequencing of the human genome was only made possible by the massively parallel use of automated high-throughput technologies. These technologies

have required the development and interfacing of new hardware and software in a way which would have been hardly conceivable only ten years ago. As a consequence, an unbroken trend to more "industrialized science" is apparent. The wealth of information generated by intensive sequencing efforts is now being further exploited by using complex tools to comprehensively analyze complex systems at the DNA, RNA and protein level. A landmark innovation was the introduction of the bio chip principle, best exemplified with the development of the ***DNA*** ***chip*** , mainly used for RNA expression profiling. The chip principle, together with miniaturization, has now become the dominating theme for a no. of new genomics and proteomics technologies, culminating in the lab-on-a-chip concept which, in the next five to ten years, could advance at a comparable rate to that of ***computers*** over the last 50 yr. Some of the new technologies are already used for comprehensive anal. of clin. samples in an attempt to describe disease and disease risk at the mol. level. However, all of these technologies are far from routine in clin. use and it is also too early to decide whether mol. fingerprints or signature profiles will have the diagnostic and prognostic power currently predicted.
RE.CNT 59 THERE ARE 59 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 5 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 2000:885245 CAPLUS
DN 135:191216
TI How to search for information about transcriptional regulation using the TRANSFAC database
AU Miyamoto, Yasunori
CS Department of Biology, Ochanomizu University, Tokyo, 112-8610, Japan
SO Trends in Glycoscience and Glycotechnology (2000), 12(67), 351-360 CODEN: TGGLEE; ISSN: 0915-7352
PB FCCA
DT Journal; General Review
LA English
AB Transcription factors regulate gene expression and are responsible for various biol. processes such as cell proliferation, cell differentiation, and apoptosis. Recently, anal. of genomes in various organisms is advancing rapidly, and technol. for the anal. of multiple gene expression such as ***DNA*** ***chip*** technol. is developing rapidly. Therefore, the necessity has arisen for many researchers in various fields to obtain information on transcription factors, which regulate gene expression. "TRANSFAC" is a database of transcription factors. In this paper, the author explains the practical and elementary operations not only of the TRANSFAC database to search for information on the transcriptional regulatory mechanism of transcription factors and genes, but also of a program, MatInspector, to predict the potential binding sites of the gene of interest.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 6 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 2000:843838 CAPLUS
DN 135:41506
TI Quantitative analysis of DNA array autoradiographs
AU Pelizzari, Charles A.; Khodarev, Nikolai N.; Gupta, Nalin; Calvin, Douglas P.; Weichselbaum, Ralph R.
CS Department of Radiation and Cellular Oncology, The University of Chicago, Chicago, IL, 60637, USA
SO Nucleic Acids Research (2000), 28(22), 4577-4581 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB ***DNA*** arrays and ***chips*** are powerful new tools for gene expression profiling. Current arrays contain hundreds or thousands of probes and large scale sequencing and screening projects will likely lead to the creation of global genomic arrays. ***DNA*** arrays and ***chips*** will be key in understanding how genes respond to specific changes of environment and will also greatly assist in drug discovery and mol. diagnostics. To facilitate widespread realization of the quant. potential of this approach, we have designed procedures and software which facilitate anal. of autoradiog. films with accuracy comparable to phosphorimaging devices. Algorithms designed for anal. of DNA array autoradiographs incorporate 3-D peak fitting of features on films and estn. of local backgrounds. This software has a flexible grid geometry and can be applied to different types of DNA arrays, including custom arrays.
RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 7 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 2000:670670 CAPLUS
DN 135:884
TI Computational simulation of bio-microfluidic processes in integrated DNA biochips
AU Przekwas, A.; Makhijani, V.; Athavale, M.; Klein, A.; Bartsch, P.
CS CFD Research Corp, Huntsville, AL, USA
SO Micro Total Analysis Systems 2000, Proceedings of the .mu.TAS Symposium, 4th, Enschede, Netherlands, May 14-18, 2000 (2000), 561-564. Editor(s): Van den Berg, Albert; Olthuis, W.; Bergveld, Piet. Publisher: Kluwer Academic Publishers, Dordrecht, Neth. CODEN: 69AJPB
DT Conference
LA English
AB Recent developments in mol. biol. and genetic anal. have inspired strong interests in miniaturization of ***DNA*** anal. on a single microfluidic ***chip*** . In the last few years there has been tremendous interest in developing a complete biochem. intelligent microsystem for extn., concn., amplification, anal., and processing of DNA. Current biochips are being developed in a very conventional exptl. trial and error manner with little computational design support. This paper presents a new software tool, CFD-ACE+, which has been developed for multidisciplinary, multiscale design of biochips. The paper describes the computational physics involved in modeling bio-microfluidic devices, and demonstrates it on a biochip for extn., concn. of DNA from fluidic samples and on PCR amplification. Other bioprocessing steps such as hybridization and electrophoretic sepn. in microfluidic networks on a chip, can also be analyzed with CFD-ACE+.
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 8 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 2000:670649 CAPLUS
DN 134:361913
TI Parallel ***DNA*** sequencing on microfabricated electrophoresis ***chips***
AU Liu, Shaorong; Ren, Hongji; Gao, Quifeng; Roach, David J.; Loder, Robert T., Jr.; Armstrong, Thomas M.; Mao, Qinglu; Blaga, Luliu; Barker, David L.; Jovanovich, Stevan B.
CS Technology Development Department, Molecular Dynamics/APB-Sunnyvale, Sunnyvale, CA, 94086, USA
SO Micro Total Analysis Systems 2000, Proceedings of the .mu.TAS Symposium, 4th, Enschede, Netherlands, May 14-18, 2000 (2000), 477-480. Editor(s): Van den Berg, Albert; Olthuis, W.; Bergveld, Piet. Publisher: Kluwer Academic Publishers, Dordrecht, Neth. CODEN: 69AJPB

DT Conference
LA English
AB We report the fabrication and applications of a 16-channel capillary array electrophoresis (CAE) ***chip*** for parallel ***DNA*** sequencing. Samples are automatically loaded into sample reservoirs using an 8-tip pipetting device. Under ***computer*** control, high voltage is applied to the appropriate reservoirs in a programmed sequence that injects and separates the DNA samples. An integrated four-color confocal fluorescent detector automatically scans all 16 channels. The system routinely yields more than 450 bases in 15 min in all 16 channels. In the best case using an automated base-calling program, 543 bases have been called at an accuracy of >99% and 608 bases at 98%. Sepns., including automated chip loading and sample injection, are normally completed in less than 18 min.
RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 9 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 2000:581083 CAPLUS
DN 134:144014
TI Automation of optical tweezers
AU Hsieh, Tseng-Ming; Chang, Bo-Jui; Hsu, Long
CS Inst. Electro-Optics, National Chiao-Tung Univ., Taiwan
SO Proceedings of SPIE-The International Society for Optical Engineering (2000), 4082(Optical Sensing, Imaging, and Manipulation for Biological and Biomedical Applications), 232-240 CODEN: PSISDG; ISSN: 0277-786X
PB SPIE-The International Society for Optical Engineering
DT Journal
LA English
AB Optical tweezers is a newly developed instrument, which makes possible the manipulation of micro-optical particles under a microscope. In this paper, we present the automation of an optical tweezers which consists of a modified optical tweezers, equipped with two motorized actuators to deflect a 1 W argon laser beam, and a ***computer*** control system including a joystick. The trapping of a single bead and a group of lactoacidofilus was shown, sep. With the aid of the joystick and two auxiliary cursors superimposed on the real-time image of a trapped bead, we demonstrated the simple and convenient operation of the automated optical tweezers. By steering the joystick and then pressing a button on it, we assign a new location for the trapped bead to move to. The increment of the motion 0.04 .mu. m for a 20X objective, is negligible. With a fast ***computer*** for image processing, the manipulation of the trapped bead is smooth and accurate. The automation of the optical tweezers is also programmable. This technique may be applied to accelerate the ***DNA*** hybridization in a gene ***chip*** . The combination of the modified optical tweezers with the ***computer*** control system provides a tool for precise manipulation of micro particles in many scientific fields.
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 10 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 2000:417809 CAPLUS
DN 134:173819
TI Gene expression analysis by DNA computing
AU Suyama, Akira; Nishida, Nao; Kurata, Ken-ichi; Omagari, Katsumi
CS Institute of Physics, University of Tokyo, Tokyo, 153-8902, Japan
SO Frontiers Science Series (2000), 30(Currents in Computational Molecular Biology), 12-13 CODEN: FCFUEO; ISSN: 0915-8502
PB Universal Academy Press, Inc.
DT Journal
LA English
AB A DNA computing (DNAC) algorithm for gene expression profiling (GEP) was developed. GEP is achieved using a universal ***DNA*** ***chip*** with a small no. of ***DNA*** probes, whose sequences have been optimized for accurate and quant. hybridization.
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 11 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 2000:372688 CAPLUS
DN 134:2298
TI Microfluidic filtration ***chip*** for ***DNA*** extraction and concentration
AU Przekwas, Agata; Wang, DeMing; Makhijani, Vinod B.; Przekwas, Andrzej J.
CS CFD Research Corp., Huntsville, AL, 35805, USA
SO Microreaction Technology: Industrial Prospects, Proceedings of the International Conference on Microreaction Technology, 3rd, Frankfurt, Apr. 18-21, 1999 (1999), 488-497. Editor(s): Ehrfeld, Wolfgang. Publisher: Springer-Verlag, Berlin, Germany. CODEN: 69BCAE
DT Conference
LA English
AB In the last few years there has been tremendous interest in developing a complete biomedical/biochem. intelligent microsystem for extn., concn., amplification, anal. and processing of DNA. This paper presents multi-disciplinary computational tool, CFD-ACE+MEMS, for simulation and design of microfluidic bioMEMS. It is demonstrated on 3D high-fidelity simulations in microfluidic channels and on a complex ***DNA*** filtration ***chip*** .
RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 12 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 2000:341489 CAPLUS
DN 133:247796
TI Automated parallel DNA sequencing on multiple channel microchips
AU Liu, Shaorong; Ren, Hongji; Gao, Qiufeng; Roach, David J.; Loder, Robert T., Jr.; Armstrong, Thomas M.; Mao, Qinglu; Blaga, Iuliu; Barker, David L.; Jovanovich, Stevan B.
CS Molecular Dynamics/Amersham Pharmacia Biotech, Sunnyvale, CA, 94086, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2000), 97(10), 5369-5374 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB We report automated DNA sequencing in 16-channel microchips. A microchip prefilled with sieving matrix is aligned on a heating plate affixed to a movable platform. Samples are loaded into sample reservoirs by using an eight-tip pipetting device, and the chip is docked with an array of electrodes in the focal plane of a four-color scanning detection system. Under ***computer*** control, high voltage is applied to the appropriate reservoirs in a programmed sequence that injects and separates the DNA samples. An integrated four-color confocal fluorescent detector automatically scans all 16 channels. The system routinely yields more than 450 bases in 15 min in all 16 channels. In the best case using an automated base-calling program, 543 bases have been called at an accuracy of >99%. Sepns., including automated chip loading and sample injection, normally are completed in less than 18 min. The advantages of ***DNA*** sequencing on capillary electrophoresis ***chips***

include uniform signal intensity and tolerance of high DNA template concn. To understand the fundamentals of these unique features we developed a theor. treatment of cross-channel chip injection that we call the differential concn. effect. We present exptl. evidence consistent with the predictions of the theory.
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 13 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 2000:244577 CAPLUS
DN 133:188557
TI Development of ***DNA*** ***chip*** microarrayer
AU Yoon, Sung Ho; Choi, Jong Gil; Lee, Sang Yup
CS Department of Chemical Engineering and BioProcess Engineering Research Center, Korea Advanced Institute of Science and Technology, Taejon, 305-701, S. Korea
SO Journal of Microbiology and Biotechnology (2000), 10(1), 21-26 CODEN: JOMBES; ISSN: 1017-7825
PB Korean Society for Applied Microbiology
DT Journal
LA English
AB A microarrayer system was developed mainly for manufg. ***DNA*** ***chips*** . The 3-axis robot was designed to automatically collect samples from 96- or 384-well microtiter plates using up to 16 simultaneously moving pens and to deposit them on a surface-modified slide glass. This is followed by a wash/dry operation in a clean station. The cycle is repeated with a new set of samples. This system can deposit cDNA or oligonucleotides with spot intervals of 150 .mu.m and the spot size of 80 .mu.m, thus allowing a high d. ***DNA*** ***chip*** contg. about 5,000 spots per cm2. The entire procedure is controlled by the Visual C++ program that was written in our lab. by using a personal ***computer*** with Pentium 100 CPU.
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 14 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 2000:151145 CAPLUS
DN 132:190484
TI ***Computer*** systems and methods of image processing for aligning scanned images
IN Fiekowski, Peter; Bartell, Dan M.
PA Affymetrix Inc., USA
SO Jpn. Kokai Tokkyo Koho, 48 pp. CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---- ---------- ---- -------- ---------- --------
PI JP 2000069998 A2 20000307 JP 1998-377796 19981209 US 6090555 A 20000718 US 1997-996737 19971223
PRAI US 1997-69032P P 19971211 US 1997-996737 A 19971223
AB ***Computer*** systems and methods of image processing are provided for aligning grids on a scanned image of a chip contg. hybridized nucleic acid sequences. A pattern is included in the scanned image so that when the image is convolved with a filter, a recognizable pattern is generated in the convolved image. The scanned image may then be aligned to the position of the recognizable pattern in the convolved image. The filter may also act to remove the portions of the scanned image that do not correspond to the pattern in the scanned image. Detailed description of the system flow diagrams is given.

L7 ANSWER 15 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 2000:145870 CAPLUS
DN 132:330385
TI ***DNA*** ***chips***
AU Delpech, M.
CS Laboratoire de biochimie et genetique moleculaire, Hopital Cochin, Faculte de medecine Cochin-Port-Royal, ICGM, Paris, 75014, Fr.
SO Annales de Biologie Clinique (2000), 58(1), 29-38 CODEN: ABCLAI; ISSN: 0003-3898
PB John Libbey Eurotext
DT Journal; General Review
LA French
AB A review with 44 refs. ***DNA*** ***chips*** represent a miniaturization of the classical system of reverse dot-blot. They consist of a small size support made of plastic or glass or silicon on which probes are synthesized or immobilized. It is thus possible to fix a few thousand or even a hundred of thousands of probes per cm2. Practically the chips are hybridized with the nucleic acid to be studied that has been amplified beforehand by PCR and which is generally labeled by a fluorochrome, either during amplification or after hybridization. After washing the hybrids are detected by a system which most of the time consists of a laser and a confocal microscope interfaced with a ***computer*** , but many variations exist. It is thus possible to analyze at the same time a considerable no. of sequences. The diagnostic applications are only at the prototype stage. Eventually the chips should allow the identification of any point mutation, or the search for bacteria, viruses or parasites in a very short period of time without preliminary cultures. They should also allow many sorts of typing ranging from infectious agents to HLA. They should become a particularly powerful tool in the search for new medicines and in the revealing of their toxicity. A considerable potential market is also the diagnosis of the predisposition to polygenic diseases or to a particular sensitivity to any chem. substance. In fact the chips are only just beginning to be used. One of the foreseeable developments should be the possibility to study nucleic acids without preliminary amplification and we can hope to eventually have at our disposal very cheap, autonomous integrated systems. The technol. could eventually extend to fields other than mol. biol. such as immunol. or biochem.
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 16 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 1999:753374 CAPLUS
DN 132:1780
TI Method and device for photolithographic production of ***DNA*** , PNA and protein ***chips***
IN Heuermann, Arno Svend
PA Epigenomics G,m,b,H., Germany
SO PCT Int. Appl., 15 pp. CODEN: PIXXD2
DT Patent
LA German
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---- ---------- ---- -------- ---------- --------
PI WO 9960156 A2 19991125 WO 1999-DE1524 19990517 WO 9960156 A3 20000217 W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG DE 19823454 A1 19991125 DE 1998-19823454 19980518 AU 9948968 A1 19991206 AU 1999-48968 19990517
PRAI DE 1998-19823454 19980518 WO 1999-DE1524 19990517
AB Disclosed is a method for photolithog. prodn. of oligonucleotides on two-dimensional matrixes for the prodn. of so-called ***DNA*** , PNA or protein ***chips*** by using

dynamically controlled liq. crystal masks as photolithog. masks. The invention also relates to a device for implementing said method. The liq. crystal masks are formed for removal of the protective groups by irradn. ***Computer*** program is used for the process control of the photochem. solid phase synthesis according to the biosequence at the different spots.

L7 ANSWER 17 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 1999:724759 CAPLUS
DN 132:176239
TI ***DNA*** ***chips*** , microarrays and genomics
AU Gupta, P. K.; Roy, Joy K.; Prasad, Manoj
CS Molecular Biology Laboratory, Department of Agricultural Botany, Ch. Charan Singh University, Meerut, 250 004, India
SO Current Science (1999), 77(7), 875-884 CODEN: CUSCAM; ISSN: 0011-3891
PB Current Science Association
DT Journal; General Review
LA English
AB A review with 30 refs. During the last few years (1995-99), genomics research has witnessed an unprecedented progress due to the availability of microarrays on ***DNA*** ***chips*** . For an organism these microarrays allow parallel acquisition of massive data for thousands/millions of specific DNA sequences, which can be analyzed using automated ***computer*** devices. The microarrays can be produced using in situ synthesis of oligonucleotides of known sequences at specific sites or by deposition, at specific sites, of DNA mols. already prepd. Robotics are used to achieve automation in the prodn. and the microarrays thus produced may involve oligonucleotides or cDNAs, that are used as probes for hybridization with labeled genomic DNA or mRNA/cDNA used as the target. These microarrays are being put to a variety of applications including the following: (i) DNA sequencing/resequencing, (ii) single nucleotide polymorphisms (SNPs), (iii) functional genomics, (iv) studies involving reverse genetics, (v) diagnostics and genetic mapping, (vi) genomic mismatch scanning (GMS), (vii) agricultural biotechnol. and (viii) proteomics. These applications of ***DNA*** ***chips*** will be realized and will expand in future for the benefit of mankind, in the fields of health care and agricultural biotechnol.
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 18 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 1999:722500 CAPLUS
DN 132:298584
TI ***DNA*** ***chip*** technology-designed antisense oligonucleotides are effective inhibitors of EGFR mRNA expression when delivered with optimised cationic lipids
AU Petch, A. K.; Sohail, M.; Southern, E.; Akhtar, S.
CS Pharmaceutical Sciences Research Institute, Aston University, Birmingham, B4 7ET, UK
SO Proceedings of the International Symposium on Controlled Release of Bioactive Materials (1999), 26th, 831-832 CODEN: PCRMEY; ISSN: 1022-0178
PB Controlled Release Society, Inc.
DT Journal
LA English
AB ***DNA*** ***chip*** technol. is capable of predicting accessible regions along any mRNA mol. of choice. It highlighted 2 accessible sites along the first 120 nucleotide length of the EGFr mRNA and from this 2 21-mer oligonucleotides were synthesized (AS1 and AS2, sequences not shown). ***Computer*** folding programs would not have predicted these sites and thus, in order to establish whether the predicted sequences were advantageous, their efficacy was tested in cell culture. A lipid delivery system was required in order for the ODN to enter the cell. With increasing doses of AS1 and AS2 in the presence of 7.5 .mu.M cationic lipid, a dose-dependent effect was obsd. There was a decrease in cell no. compared to control-treated cells of 60% at 0.5 .mu.M, but further increases in dose did not increase the effect.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 19 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 1999:683615 CAPLUS
DN 132:45502
TI Maskless fabrication of light-directed oligonucleotide microarrays using a digital micromirror array
AU Singh-Gasson, Sangeet; Green, Roland D.; Yue, Yongjian; Nelson, Clark; Blattner, Fred; Sussman, Michael R.; Cerrina, Franco
CS Cent. NanoTechnol., Dep. Electrical and Computer Eng., Univ. Wisconsin, Madison, WI, 53706, USA
SO Nature Biotechnology (1999), 17(10), 974-978 CODEN: NABIF9; ISSN: 1087-0156
PB Nature America
DT Journal
LA English
AB Oligonucleotide microarrays, also called " ***DNA*** ***chips*** ," are currently made by a light-directed chem. that requires a large no. of photolithog. masks for each chip. Here we describe a maskless array synthesizer (MAS) that replaces the chrome masks with virtual masks generated on a ***computer*** , which are relayed to a digital micromirror array. A 1:1 reflective imaging system forms an UV image of the virtual mask on the active surface of the glass substrate, which is mounted in a flow cell reaction chamber connected to a DNA synthesizer. Programmed chem. coupling cycles follow light exposure, and these steps are repeated with different virtual masks to grow desired oligonucleotides in a selected pattern. This instrument has been used to synthesize oligonucleotide microarrays contg. more than 76,000 features measuring 16 .mu.m2. The oligonucleotides were synthesized at high repetitive yield and, after hybridization, could readily discriminate single-base pair mismatches. The MAS is adaptable to the fabrication of ***DNA*** ***chips*** contg. probes for thousands of genes, as well as any other solid-phase combinatorial chem. to be performed in high-d. microarrays.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 20 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 1999:669133 CAPLUS
DN 132:91127
TI Potassium ATPases, channels, and transporters: an overview
AU Meneton, Pierre; Lesage, Florian; Barhanin, Jacques
CS INSERM U367, Paris, 75005, Fr.
SO Seminars in Nephrology (1999), 19(5), 438-457 CODEN: SNEPDJ; ISSN: 0270-9295
PB W. B. Saunders Co.
DT Journal; General Review
LA English
AB A review with 164 refs. The identification of multigene families encoding K-ATPases, K channels, and K transporters is a major step in understanding the mol. mechanisms engaged in K homeostasis. These membrane proteins, which also transport Na, H, or Cl ions, have been shown to play fundamental roles in cellular housekeeping functions (vol. regulation, uptake of nutrients) and in specialized tissue functions (transepithelial transport of solutes and water, uptake of neurotransmitters, control of vascular tone). The assocn. of mutations (esp. in the K channels) with human diseases and disorders as well as the

creation of animal models harboring specific gene inactivation should allow investigators to reach nonambiguous conclusions about the roles of these genes. These approaches should be complemented by techniques such as ***DNA*** array and ***chip*** hybridization and ***computer*** -based simulation in order to form an integrated view of the functional interactions between the genes underlying physiol. and pathol. processes.
RE.CNT 166 THERE ARE 166 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 21 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 1999:202375 CAPLUS
DN 131:2357
TI Ultratrace Measurements of Nucleic Acids by Baseline-Corrected Adsorptive Stripping Square-Wave Voltammetry
AU Wang, Joseph; Bollo, Soledad; Lopez Paz, Jose Luis; Sahlin, Eskil; Mukherjee, Baidehi
CS Department of Chemistry and Biochemistry, New Mexico State University, Las Cruces, NM, 88003, USA
SO Analytical Chemistry (1999), 71(9), 1910-1913 CODEN: ANCHAM; ISSN: 0003-2700
PB American Chemical Society
DT Journal
LA English
AB The direct and reliable electrochem. detection of DNA is of paramount importance to the development of modern ***DNA*** hybridization ***chips*** , for the detection of nucleic acids following their electrophoretic sepns., or for the sensing of DNA damage and interactions. Such solid electrode voltammetric measurements of nucleic acids have been traditionally hampered by the large solvent decompn. background current that obscures the oxidn. signals of the purine nucleobases. This paper reports on the use of adsorptive stripping square-wave voltammetry, in connection with the "moving av. baseline correction" approach, for monitoring ultratrace levels of DNA and RNA. Compared to other baseline-fitted or background-subtraction protocols, the moving av. baseline scheme is particularly effective in isolating the small purine nucleobase peaks, which appear as small shoulders on the steep background discharge contribution. The remarkably flat baseline thus obtained (up to extreme potentials) leads to a dramatic lowering of the detection limits to the femtomole level and to a performance that compares favorably with that of ***computerized*** chronopotentiometric measurements of nucleic acids. Combined with the speed of square-wave voltammetric measurements, such developments should expand the role of voltammetry in DNA diagnostics and nucleic acid research.
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 22 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 1999:198138 CAPLUS
DN 131:68568
TI Genetics of proteome variation for QTL characterization: application to drought-stress responses in maize
AU De Vienne, Dominique; Leonardi, Agnes; Damerval, Catherine; Zivy, Michel
CS Station de Genetique Vegetale, INRA/UPS/INA PG/CNRS URA 2154, Ferme du Moulon, Gif-sur-Yvette, 91190, Fr.
SO Journal of Experimental Botany (1999), 50(332), 303-309 CODEN: JEBOA6; ISSN: 0022-0957
PB Oxford University Press
DT Journal; General Review
LA English
AB A review with 55 refs. The proteome is emerging as an important concept of the post-genome era. Powerful nucleic acid approaches (EST, ***DNA*** ***chips*** , etc.) are still limited because ***DNA*** sequences and mRNA levels are not sufficient to predict the structure, function, amt., and activity of the proteins in the cell. The proteome can now be subjected to large-scale anal., owing to spectacular progress in the techniques of identification of proteins excised from two-dimensional (2-D) gels. In addn., ***computer*** -based anal. of 2-D gels makes it possible to quantify the protein spot intensities, which are commonly genetically variable. The loci controlling these variations may be mapped on the genome (PQLs, Protein Quantity Loci). Beyond the interest for regulatory genetics and mol. biol., the PQL methodol. can provide an addnl. tool for the difficult task of identifying QTLs (Quant. Trait Loci), in the context of the candidate gene approach. The PQL methodol. is presented with the example of the phosphoglycerate mutase variations in maize, and the candidate gene/protein approach is illustrated for traits responsive to drought stress.
RE.CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 23 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 1999:10742 CAPLUS
DN 130:247468
TI A new diagnostic tool in medical genetics: The ***DNA*** - ***chip***
AU Kiss, A.; Karabelyos, Cs.; Falus, A.
CS Seminelweis Orvostudomanyi Egyetem, Genetikai, Sejt-es Immunobiological Intezet, Budapest, 1085, Hung.
SO Gyogyszereszet (1998), 42(10), 531-534 CODEN: GYOGAI; ISSN: 0017-6036
PB Gyogyszereszet Szerkesztosege
DT Journal; General Review
LA Hungarian
AB A review with 12 refs. The ***DNA*** (gene)- ***chip*** technol., emerged in the last two years, provides an incredible tech. development in performance of genetic identification, markedly decreased the duration of the investigations, and simplified their procedure. The principle of procedure is, that by series of photolithog. and chem. steps on solid-phase of a small surface relatively dense oligonucleotide (in a lot of variation) arrays can be generated. The oligonucleotides produced by the ***computer*** -directed in situ microfabrication may bind complementary fluorescent-labeled DNA fragments from the unknown samples; after scanning the registered position of pos. signals provide information on the identity of DNA fragments. By this novel approach not only the DNA sequencing can be performed, but it is suitable in other fields of medical and pharmaceutical sciences (identification of genetic defects, confirmation of the presence of microorganisms, in view of detn. of the right therapy, application in the synthetic pharmacy, screening of transplantations-incompatibility, forensic medicine, etc.).

L7 ANSWER 24 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 1998:455323 CAPLUS
DN 129:185050
TI GeneUp: a program to select short PCR primer pairs that occur in multiple members of sequence lists
AU Pesole, G.; Liuni, S.; Grillo, G.; Belichard, P.; Trenkle, T.; Welsh, J.; McClelland, M.
CS Univ. Basilicata, Potenza, Italy
SO BioTechniques (1998), 25(1), 112-117, 120-123 CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal

LA English
AB A ***computer*** program is presented that selects a small set of short primer pairs for PCR to sample all the sequences in a user-specified list of mRNAs. Such primer pairs could be used to increase the probability of sampling mRNAs of particular interest in differential display and to generate simplified hybridization probes for ***DNA*** ***chips*** or arrays. The program uses simulated PCR to find pairs of primers that sample more than one sequence in the list. A small set of such primer pairs is selected that give maximal coverage of the sequences in the list. Primer pairs are excluded that: (i) generate simulated PCR products of the same size from a no.of sequences in the list, (ii) can easily form primer dimers, (iii) are outside a specified range of G+C content or (i.v.) occur in another list of undesirable sequences, such as rRNAs and Alu repeats. Five lists consisting of from 48-285 cDNA sequences were used to test the program. A small no. of pairs of primers, 8-10 bases in length, were selected that fit the above criteria and that generate one or more simulated PCR products in all or most of the cDNAS in each list.

L7 ANSWER 25 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 1997:787249 CAPLUS
DN 128:98214
TI Quantitation of the Escherichia coli methionine repressor-operator interaction by surface plasmon resonance is not affected by the presence of a dextran matrix
AU Parsons, Isobel D.; Stockley, Peter G.
CS School of Biology, University of Leeds, Leeds, LS2 9JT, UK
SO Analytical Biochemistry (1997), 254(1), 82-87 CODEN: ANBCA2; ISSN: 0003-2697
PB Academic Press
DT Journal
LA English
AB The effect of a dextran matrix on the apparent rate consts. measured for the interaction of the Escherichia coli methionine repressor, MetJ, with its immobilized consensus operator has been studied using surface plasmon resonance (SPR) in a com. biosensor, BIACORE (Biacore AB). Based on the results of ***computer*** simulations, it has been proposed that such data can deviate from the expected simple kinetic behavior due to effects generated by the dextran matrix, used at the biosensor surface to anchor one of the interacting mols. We have tested this possibility exptl. by measuring the apparent rate consts. for the interaction of MetJ with its operator ***DNA*** on sensor ***chip*** surfaces with no dextran matrix or having matrixes 30 or 100 nm thick. The data show that for the MetJ-operator interaction, the dextran matrix has no significant effect on the apparent rate consts. measured and that comparative measurements using this technique are informative.

L7 ANSWER 26 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 1997:678976 CAPLUS
DN 127:315569
TI Selecting tag nucleic acids and probe arrays for very large scale immobilized polymer synthesis and hybridization
IN Morris, MacDonald S.; Schoemaker, Daniel D.; Davis, Ronald W.; Mittmann, Michael P.
PA Affymetrix, Inc., USA
SO Eur. Pat. Appl., 46 pp. CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---- ---------- ---- -------- ---------- --------
PI EP 799897 A1 19971008 EP 1997-302313 19970403 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI
PRAI US 1996-626285 19960404
AB Methods and criteria for selecting nucleic acid tags, e.g. for the monitoring of patterns of gene expression, for use in hybridization against very large arrays of immobilized probes are described. Sequences are selected by criteria including the lack of hairpins, lack of runs of >4 identical bases and elimination of common nonamers. Algorithms for design of unique tags with minimal cross hybridization are described.

L7 ANSWER 27 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 1997:125938 CAPLUS
DN 126:181810
TI Microfabrication and array technologies for DNA sequencing and diagnostics
AU O'Donnell-Maloney, Maryanne J.; Little, Daniel P.
CS Sequenom Inc., Boston, MA, 02110, USA
SO Genetic Analysis: Biomolecular Engineering (1996), 13(6), 151-157 CODEN: GEANF4
PB Elsevier
DT Journal; General Review
LA English
AB A review with 18 refs. It is now possible to miniaturize numerous "macroscale" processes and develop microfabricated devices to replace conventional equipment. Such advances have lead to the development of arrays of immobilized oligonucleotides useful for basic research, diagnostic studies, sequence anal. and a no. of novel applications. Addnl., std. lab. equipment has been redesigned on a microscale level to increase efficiency; many processes have been integrated onto one chip since miniaturization can be readily achieved.

L7 ANSWER 28 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 1997:95178 CAPLUS
DN 126:153198
TI ***DNA*** sequencing on a ***chip***
AU Wallraff, G.; Labadie, J.; Brock, P.; DiPietro, R.; Nguyen, T.; Huynh, T.; Hinsberg, W.; McGall, G.
CS IBM Almaden Res. Cent., USA
SO CHEMTECH (1997), 27(2), 22-32 CODEN: CHTEDD; ISSN: 0009-2703
PB American Chemical Society
DT Journal; General Review
LA English
AB A review with 23 refs. We have devised two new methods for the fabrication of high-d. oligonucleotide arrays. In the first, we use polymeric photoresists to make arrays using std. DMT-protected nucleoside phosphoramidites and conventional semiconductor lithog. tools. We created 8-.mu.m features and anticipate higher resoln. with further process optimization. Test arrays display hybridization characteristics equiv. to those prepd. using previously reported techniques. In the second approach, we use photogenerated acid in solid polymer thin-film matrixes to spatially direct the detritylation of substrate-bound DMT-protected oligonucleotides (the PPA process). We have obsd. reasonably efficient oligonucleotide synthesis for thymidine oligomers made using strong photoacids such as triflic acid as the detritylation catalyst. At present, depurination of adenosine groups limits the general utility of this method. We demonstrated resoln. of 10-.mu.m features and hybridization with decamers in which one nucleotide was introduced using the PPA method.

L7 ANSWER 29 OF 29 CAPLUS COPYRIGHT 2002 ACS
AN 1994:20222 CAPLUS
DN 120:20222
TI ***DNA*** technology in ***chip*** construction
AU Di Mauro, Ernesto; Hollenberg, Cornelis P.
CS Dip. Genet. Biol. Mol., Univ. Sapienza, Rome, Italy

SO Advanced Materials (Weinheim, Germany) (1993), 5(5), 384-6
CODEN: ADVMEW; ISSN: 0935-9648
DT Journal; General Review
LA English
AB A review with 5 refs. Topics include: construction of nucleic acid networks, conversion of a nucleic acid or nucleic acid-protein network to an electronic microcircuit, and photolithog. using DNA as a mask.

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